

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Koji YANAI et al.
- (ii) TITLE OF INVENTION: β -FRUCTOFURANOSIDASE AND ITS GENE,
METHOD OF ISOLATING β -FRUCTOFURANOSIDASE GENE, SYSTEM
FOR PRODUCING β -FRUCTOFURANOSIDASE, AND
 β -FRUCTOFURANOSIDASE VARIANT
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 - (B) STREET: 2033 K Street, N.W., Suite 800
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20006
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: MS-DOS
 - (D) SOFTWARE: Wordperfect 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: NEW
 - (B) FILING DATE: November 23, 2001
- (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/142,623

(B) FILING DATE: September 10, 1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lee Cheng

(B) REGISTRATION NUMBER: 40,949

(C) REFERENCE/DOCKET NUMBER: 2001-1611

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-721-8200

(B) TELEFAX: 202-721-8250

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 amino acid residues

(B) TYPE: amino acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: Not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1

(ATCC 20611)

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1..635

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser Tyr His Leu Asp Thr Thr Ala Pro Pro Pro Thr Asn Leu Ser Thr
1 5 10 15

Leu Pro Asn Asn Thr Leu Phe His Val Trp Arg Pro Arg Ala His Ile
20 25 30

Leu Pro Ala Glu Gly Gln Ile Gly Asp Pro Cys Ala His Tyr Thr Asp
35 40 45

Pro Ser Thr Gly Leu Phe His Val Gly Phe Leu His Asp Gly Asp Gly
50 55 60

Ile Ala Gly Ala Thr Thr Ala Asn Leu Ala Thr Tyr Thr Asp Thr Ser
65 70 75 80

Asp Asn Gly Ser Phe Leu Ile Gln Pro Gly Gly Lys Asn Asp Pro Val
85 90 95

Ala Val Phe Asp Gly Ala Val Ile Pro Val Gly Val Asn Asn Thr Pro
100 105 110

Thr Leu Leu Tyr Thr Ser Val Ser Phe Leu Pro Ile His Trp Ser Ile
115 120 125

Pro Tyr Thr Arg Gly Ser Glu Thr Gln Ser Leu Ala Val Ala Arg Asp
130 135 140

Gly Gly Arg Arg Phe Asp Lys Leu Asp Gln Gly Pro Val Ile Ala Asp
145 150 155 160

His Pro Phe Ala Val Asp Val Thr Ala Phe Arg Asp Pro Phe Val Phe
165 170 175

Arg Ser Ala Lys Leu Asp Val Leu Leu Ser Leu Asp Glu Glu Val Ala
180 185 190

Arg Asn Glu Thr Ala Val Gln Gln Ala Val Asp Gly Trp Thr Glu Lys
195 200 205

Asn Ala Pro Trp Tyr Val Ala Val Ser Gly Gly Val His Gly Val Gly
210 215 220

Pro Ala Gln Phe Leu Tyr Arg Gln Asn Gly Gly Asn Ala Ser Glu Phe
225 230 235 240

Gln Tyr Trp Glu Tyr Leu Gly Glu Trp Trp Gln Glu Ala Thr Asn Ser
245 250 255

Ser Trp Gly Asp Glu Gly Thr Trp Ala Gly Arg Trp Gly Phe Asn Phe
260 265 270

Glu Thr Gly Asn Val Leu Phe Leu Thr Glu Glu Gly His Asp Pro Gln
275 280 285

Thr Gly Glu Val Phe Val Thr Leu Gly Thr Glu Gly Ser Gly Leu Pro
290 295 300

Ile Val Pro Gln Val Ser Ser Ile His Asp Met Leu Trp Ala Ala Gly
305 310 315 320

Glu Val Gly Val Gly Ser Glu Gln Glu Gly Ala Lys Val Glu Phe Ser
325 330 335

Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser Ala Tyr Ala Ala
340 345 350

Ala Gly Lys Val Leu Pro Ala Ser Ser Ala Val Ser Lys Thr Ser Gly
355 360 365

Val Glu Val Asp Arg Tyr Val Ser Phe Val Trp Leu Thr Gly Asp Gln
370 375 380

Tyr Glu Gln Ala Asp Gly Phe Pro Thr Ala Gln Gln Gly Trp Thr Gly
385 390 395 400
Ser Leu Leu Leu Pro Arg Glu Leu Lys Val Gln Thr Val Glu Asn Val
405 410 415
Val Asp Asn Glu Leu Val Arg Glu Glu Gly Val Ser Trp Val Val Gly
420 425 430
Glu Ser Asp Asn Gln Thr Ala Arg Leu Arg Thr Leu Gly Ile Thr Ile
435 440 445
Ala Arg Glu Thr Lys Ala Ala Leu Leu Ala Asn Gly Ser Val Thr Ala
450 455 460
Glu Glu Asp Arg Thr Leu Gln Thr Ala Ala Val Val Pro Phe Ala Gln
465 470 475 480
Ser Pro Ser Ser Lys Phe Phe Val Leu Thr Ala Gln Leu Glu Phe Pro
485 490 495
Ala Ser Ala Arg Ser Ser Pro Leu Gln Ser Gly Phe Glu Ile Leu Ala
500 505 510
Ser Glu Leu Glu Arg Thr Ala Ile Tyr Tyr Gln Phe Ser Asn Glu Ser
515 520 525
Leu Val Val Asp Arg Ser Gln Thr Ser Ala Ala Ala Pro Thr Asn Pro
530 535 540
Gly Leu Asp Ser Phe Thr Glu Ser Gly Lys Leu Arg Leu Phe Asp Val
545 550 555 560
Ile Glu Asn Gly Gln Glu Gln Val Glu Thr Leu Asp Leu Thr Val Val
565 570 575

Val Asp Asn Ala Val Val Glu Val Tyr Ala Asn Gly Arg Phe Ala Leu
580 585 590
Ser Thr Trp Ala Arg Ser Trp Tyr Asp Asn Ser Thr Gln Ile Arg Phe
595 600 605
Phe His Asn Gly Glu Gly Glu Val Gln Phe Arg Asn Val Ser Val Ser
610 615 620
Glu Gly Leu Tyr Asn Ala Trp Pro Glu Arg Asn
625 630 635

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1905 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double stranded
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Aspergillus niger* ACE-2-1
(ATCC 20611)

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1 .. 1905
- (C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCATACCACC TGGACACCAAC GGCCCCGCCG CCGACCAACC TCAGCACCCCT CCCCAACAAC 60
 ACCCTCTTCC ACGTGTGGCG GCCGCGCGCG CACATCCTGC CCGCCGAGGG CCAGATCGC 120
 GACCCCTGCG CGCACTACAC CGACCCATCC ACCGGCCTCT TCCACGTGGG GTTCCTGCAC 180
 GACGGGGACG GCATCGCGGG CGCCACCACG GCCAACCTGG CCACCTACAC CGATACCTCC 240
 GATAACGGGA GCTTCCTGAT CCAGCCGGGC GGGAAAGAACG ACCCCGTCGC CGTGTTCGAC 300
 GGCGCCGTCA TCCCCGTCGG CGTCAACAAC ACCCCCACCT TACTCTACAC CTCCGTCTCC 360
 TTCCTGCCA TCCACTGGTC CATCCCCTAC ACCCGCGGCA GCGAGACGCA GTCGTTGCC 420
 GTCGCGCGCG ACGGCGGCCG CCGCTTCGAC AAGCTCGACC AGGGCCCCGT CATCGCCGAC 480
 CACCCCTTCG CCGTCGACGT CACCGCCTTC CGCGATCCGT TTGTCTTCCG CAGTGCCAAG 540
 TTGGATGTGC TGCTGTCGTT GGATGAGGAG GTGGCGCGGA ATGAGACGGC CGTGCAGCAG 600
 GCCGTCGATG GCTGGACCGA GAAGAACGCC CCCTGGTATG TCGCGGTCTC TGGCGGGGTG 660
 CACGGCGTCG GGCCCCCGCA GTTCCTCTAC CGCCAGAACG GCGGGAACGC TTCCGAGTTC 720
 CAGTACTGGG AGTACCTCGG GGAGTGGTGG CAGGAGGCGA CCAACTCCAG CTGGGGCGAC 780
 GAGGGCACCT GGGCCGGCG CTGGGGGTT AACTTCGAGA CGGGGAATGT GCTCTTCCTC 840
 ACCGAGGAGG GCCATGACCC CCAGACGGGC GAGGTGTTCG TCACCCCTCGG CACGGAGGGG 900
 TCTGGCCTGC CAATCGTGCC GCAGGTCTCC AGTATCCACG ATATGCTGTG GGCGCGGGT 960
 GAGGTGGGG TGCGCAGTGA GCAGGAGGGT GCCAAGGTCG AGTTCTCCCC CTCCATGGCC 1020
 GGGTTCTGG ACTGGGGGTT CAGCGCCTAC GCTGCGCGG GCAAGGTGCT GCCGGCCAGC 1080
 TCGCGGTGT CGAAGACCAG CGGCGTGGAG GTGGATCGGT ATGTCTCGTT CGTCTGGTTG 1140
 ACGGGCGACC AGTACGAGCA GGCAGACGGG TTCCCCACGG CCCAGCAGGG GTGGACGGGG 1200
 TCGCTGCTGC TGCCGCGCGA GCTGAAGGTG CAGACGGTGG AGAACGTCGT CGACAACCGAG 1260
 CTGGTGGCGCG AGGAGGGCGT GTCGTGGGTG GTGGGGGAGT CGGACAACCA GACGGCCAGG 1320
 CTGCGCACGC TGGGGATCAC GATCGCCCGG GAGACCAAGG CGGCCCTGCT GGCCAACGGC 1380
 TCGGTGACCG CGGAGGAGGA CCGCACGCTG CAGACGGCGG CCGTCGTGCC GTTCGCGCAA 1440
 TCGCCGAGCT CCAAGTTCTT CGTGCTGACG GCCCAGCTGG AGTTCCCCGC GAGCGCGCGC 1500

TCGTCCCCGC TCCAGTCCGG GTTCGAAATC CTGGCGTCGG AGCTGGAGCG CACGGCCATC 1560
TACTACCAGT TCAGCAACGA GTCGCTGGTC GTCGACCGCA GCCAGACTAG TGCGGCGGCG 1620
CCCACGAACC CCGGGCTGGA TAGCTTACT GAGTCCGGCA AGTTGCGGTT GTTCGACGTG 1680
ATCGAGAACG GCCAGGAGCA GGTCGAGACG TTGGATCTCA CTGTCGTCGT GGATAACGCG 1740
GTTGTCGAGG TGTATGCCAA CGGGCGCTTT GCGTTGAGCA CCTGGGCGAG ATCGTGGTAC 1800
GACAACCTCCA CCCAGATCCG CTTCTTCCAC AACGGCGAGG GCGAGGTGCA GTTCAGGAAT 1860
GTCTCCGTGT CGGAGGGGCT CTATAACGCC TGGCCGGAGA GAAAT 1905

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Asp Gln Gly Pro Val Ile Ala Asp His Pro Phe Ala Val Asp Val

1 5 10 15

Thr Ala Phe Arg

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Glu Phe Ser Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser

1

5

10

15

Ala Tyr Ala Ala

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val Gln Thr Val Glu Asn Val Val Asp Asn Glu Leu Val Arg Glu Glu
1 5 10 15
Gly Val Ser Trp
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Ala Leu Leu Ala Xaa Gly Ser Val Thr Ala Glu Glu Asp Arg Thr
1 5 10 15
Leu Gln Thr Ala
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
(ATCC 20611)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Tyr His Leu Asp Thr

1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATCGCSGAYC AYCCSTTYGC 20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCRTTRTCSA CSACRTTYTC 20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double stranded
- (D) TOPOLOGY: Linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: Aspergillus niger ACE-2-1
(ATCC 20611)

(ix) FEATURE:

- (A) NAME/KEY: P CDS(partial amino acid sequence)
- (B) LOCATION: 1 .. 788
- (C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATC	GCC	GAC	CAC	CCC	TTC	GCC	GTC	GAC	GTC	ACC	GCC	TTC	CGC	GAT	CCG	48
Ile	Ala	Asp	His	Pro	Phe	Ala	Val	Asp	Val	Thr	Ala	Phe	Arg	Asp	Pro	
1	5							10						15		
TTT	GTC	TTC	CGC	AGT	GCC	AAG	TTG	GAT	GTG	CTG	CTG	TCG	TTG	GAT	GAG	96
Phe	Val	Phe	Arg	Ser	Ala	Lys	Leu	Asp	Val	Leu	Leu	Ser	Leu	Asp	Glu	
20								25						30		
GAG	GTG	GCG	CGG	AAT	GAG	ACG	GCC	GTG	CAG	CAG	GCC	GTC	GAT	GGC	TGG	144
Glu	Val	Ala	Arg	Asn	Glu	Thr	Ala	Val	Gln	Gln	Ala	Val	Asp	Gly	Trp	
35								40						45		
ACC	GAG	AAG	AAC	GCC	CCC	TGG	TAT	GTC	GCG	GTC	TCT	GGC	GGG	GTG	CAC	192
Thr	Glu	Lys	Asn	Ala	Pro	Trp	Tyr	Val	Ala	Val	Ser	Gly	Gly	Val	His	
50								55						60		
GGC	GTC	GGG	CCC	GCG	CAG	TTC	CTC	TAC	CGC	CAG	AAC	GGC	GGG	AAC	GCT	240
Gly	Val	Gly	Pro	Ala	Gln	Phe	Leu	Tyr	Arg	Gln	Asn	Gly	Gly	Asn	Ala	
65								70						75		80
TCC	GAG	TTC	CAG	TAC	TGG	GAG	TAC	CTC	GGG	GAG	TGG	TGG	CAG	GAG	GCG	288
Ser	Glu	Phe	Gln	Tyr	Trp	Glu	Tyr	Leu	Gly	Glu	Trp	Trp	Gln	Glu	Ala	
85								90						95		
ACC	AAC	TCC	AGC	TGG	GGC	GAC	GAG	GGC	ACC	TGG	GCC	GGG	CGC	TGG	GGG	336
Thr	Asn	Ser	Ser	Trp	Gly	Asp	Glu	Gly	Thr	Trp	Ala	Gly	Arg	Trp	Gly	
100								105						110		
TTC	AAC	TTC	GAG	ACG	GGG	AAT	GTG	CTC	TTC	CTC	ACC	GAG	GAG	GGC	CAT	384
Phe	Asn	Phe	Glu	Thr	Gly	Asn	Val	Leu	Phe	Leu	Thr	Glu	Glu	Gly	His	
115								120						125		

GAC CCC CAG ACG GGC GAG GTG TTC GTC ACC CTC GGC ACG GAG GGG TCT 432
 Asp Pro Gln Thr Gly Glu Val Phe Val Thr Leu Gly Thr Glu Gly Ser
 130 135 140
 GGC CTG CCA ATC GTG CCG CAG GTC TCC AGT ATC CAC GAT ATG CTG TGG 480
 Gly Leu Pro Ile Val Pro Gln Val Ser Ser Ile His Asp Met Leu Trp
 145 150 155 160
 GCG GCG GGT GAG GTC GGG GTG GGC AGT GAG CAG GAG GGT GCC AAG GTC 528
 Ala Ala Gly Glu Val Gly Val Gly Ser Glu Gln Glu Gly Ala Lys Val
 165 170 175
 GAG TTC TCC CCC TCC ATG GCC GGG TTT CTG GAC TGG GGG TTC AGC GCC 576
 Glu Phe Ser Pro Ser Met Ala Gly Phe Leu Asp Trp Gly Phe Ser Ala
 180 185 190
 TAC GCT GCG GCG GGC AAG GTG CTG CCG GCC AGC TCG GCG GTG TCG AAG 624
 Tyr Ala Ala Ala Gly Lys Val Leu Pro Ala Ser Ser Ala Val Ser Lys
 195 200 205
 ACC AGC GGC GTG GAG GTG GAT CGG TAT GTC TCG TTC GTC TGG TTG ACG 672
 Thr Ser Gly Val Glu Val Asp Arg Tyr Val Ser Phe Val Trp Leu Thr
 210 215 220
 GGC GAC CAG TAC GAG CAG GCG GAC GGG TTC CCC ACG GCC CAG CAG GGG 720
 Gly Asp Gln Tyr Glu Gln Ala Asp Gly Phe Pro Thr Ala Gln Gln Gly
 225 230 235 240
 TGG ACG GGG TCG CTG CTG CCG CGC GAG CTG AAG GTG CAG ACG GTG 768
 Trp Thr Gly Ser Leu Leu Leu Pro Arg Glu Leu Lys Val Gln Thr Val
 245 250 255

GAG AAC GTC GTC GAC AAC GA

788

Glu Asn Val Val Asp Asn

260

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: Penicillium roqueforti IAM7254

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1 .. 565
- (C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val Asp Phe His Thr Pro Ile Asp Tyr Asn Ser Ala Pro Pro Asn Leu

1 5 10 15

Ser Thr Leu Ala Asn Ala Ser Leu Phe Lys Thr Trp Arg Pro Arg Ala

20 25 30

His Leu Leu Pro Pro Ser Gly Asn Ile Gly Asp Pro Cys Gly His Tyr

35 40 45

Thr Asp Pro Lys Thr Gly Leu Phe His Val Gly Trp Leu Tyr Ser Gly
50 55 60

Ile Ser Gly Ala Thr Thr Asp Asp Leu Val Thr Tyr Lys Asp Leu Asn
65 70 75 80

Pro Asp Gly Ala Pro Ser Ile Val Ala Gly Gly Lys Asn Asp Pro Leu
85 90 95

Ser Val Phe Asp Gly Ser Val Ile Pro Ser Gly Ile Asp Gly Met Pro
100 105 110

Thr Leu Leu Tyr Thr Ser Val Ser Tyr Leu Pro Ile His Trp Ser Ile
115 120 125

Pro Tyr Thr Arg Gly Ser Glu Thr Gln Ser Leu Ala Val Ser Tyr Asp
130 135 140

Gly Gly His Asn Phe Thr Lys Leu Asn Gln Gly Pro Val Ile Pro Thr
145 150 155 160

Pro Pro Phe Ala Leu Asn Val Thr Ala Phe Arg Asp Pro Tyr Val Phe
165 170 175

Gln Ser Pro Ile Leu Asp Lys Ser Val Asn Ser Thr Gln Gly Thr Trp
180 185 190

Tyr Val Ala Ile Ser Gly Gly Val His Gly Val Gly Pro Cys Gln Phe
195 200 205

Leu Tyr Arg Gln Asn Asp Ala Asp Phe Gln Tyr Trp Glu Tyr Leu Gly
210 215 220

Gln Trp Trp Lys Glu Pro Leu Asn Thr Thr Trp Gly Lys Gly Asp Trp
225 230 235 240

Ala Gly Gly Trp Gly Phe Asn Phe Glu Val Gly Asn Val Phe Ser Leu
245 . 250 255

Asn Ala Glu Gly Tyr Ser Glu Asp Gly Glu Ile Phe Ile Thr Leu Gly
260 265 270

Ala Glu Gly Ser Gly Leu Pro Ile Val Pro Gln Val Ser Ser Ile Arg
275 280 285

Asp Met Leu Trp Val Thr Gly Asn Val Thr Asn Asp Gly Ser Val Thr
290 295 300

Phe Lys Pro Thr Met Ala Gly Val Leu Asp Trp Gly Val Ser Ala Tyr
305 310 315 320

Ala Ala Ala Gly Lys Ile Leu Pro Ala Ser Ser Gln Ala Ser Thr Lys
325 330 335

Ser Gly Ala Pro Asp Arg Phe Ile Ser Tyr Val Trp Leu Thr Gly Asp
340 345 350

Leu Phe Glu Gln Val Lys Gly Phe Pro Thr Ala Gln Gln Asn Trp Thr
355 360 365

Gly Ala Leu Leu Leu Pro Arg Glu Leu Asn Val Arg Thr Ile Ser Asn
370 375 380

Val Val Asp Asn Glu Leu Ser Arg Glu Ser Leu Thr Ser Trp Arg Val
385 390 395 400

Ala Arg Glu Asp Ser Gly Gln Ile Asp Leu Glu Thr Met Gly Ile Ser
405 410 415

Ile Ser Arg Glu Thr Tyr Ser Ala Leu Thr Ser Gly Ser Ser Phe Val
420 425 430

Glu Ser Gly Lys Thr Leu Ser Asn Ala Gly Ala Val Pro Phe Asn Thr
435 440 445
Ser Pro Ser Ser Lys Phe Phe Val Leu Thr Ala Asn Ile Ser Phe Pro
450 455 460
Thr Ser Ala Arg Asp Ser Gly Ile Gln Ala Gly Phe Gln Val Leu Ser
465 470 475 480
Ser Ser Leu Glu Ser Thr Thr Ile Tyr Tyr Gln Phe Ser Asn Glu Ser
485 490 495
Ile Ile Val Asp Arg Ser Asn Thr Ser Ala Ala Ala Arg Thr Thr Ala
500 505 510
Gly Ile Leu Ser Asp Asn Glu Ala Gly Arg Leu Arg Leu Phe Asp Val
515 520 525
Leu Arg Asn Gly Lys Glu Gln Val Glu Thr Leu Glu Leu Thr Ile Val
530 535 540
Val Asp Asn Ser Val Leu Glu Val Tyr Ala Asn Gly Arg Phe Ala Leu
545 550 555 560
Gly Thr Trp Ala Arg
565

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1695 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double stranded
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: *Penicillium roqueforti* IAM7254

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1 .. 1695

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTGATTTCC	ATACCCCCGAT	TGACTATAAC	TCGGCTCCGC	CAAACCTTTC	TACCCTGGCA	60
AACGCATCTC	TTTCAAGAC	ATGGAGACCC	AGAGCCCATC	TTCTCCCTCC	ATCTGGGAAC	120
ATAGGCAGACC	CGTGCGGGCA	CTATACCGAT	CCCAAGACTG	GTCTCTTCCA	CGTGGGTTGG	180
CTTTACAGTG	GGATTCGGG	AGCGACAACC	GACGATCTCG	TTACCTATAA	AGACCTCAAT	240
CCCGATGGAG	CCCCGTCAAT	TGTTGCAGGA	GGAAAGAACG	ACCCTTTTC	TGTCTTCGAT	300
GGCTCGGTCA	TTCCAAGCGG	TATAGACGGC	ATGCCAACTC	TTCTGTATAC	CTCTGTATCA	360
TACCTCCCAA	TCCACTGGTC	CATCCCCTAC	ACCCGGGGAA	GCGAGACACA	ATCCTTGGCC	420
GTTCCTATG	ACGGTGGTCA	CAACTTCACC	AAGCTCAACC	AAGGGCCCGT	GATCCCTACG	480
CCTCCGTTTG	CTCTCAATGT	CACCGCTTTC	CGTGACCCCT	ACGTTTCCA	AAGCCCAATT	540
CTGGACAAAT	CTGTCAATAG	TACCCAAGGA	ACATGGTATG	TCGCCATATC	TGGCGGTGTC	600
CACGGTGTCA	GACCTTGTCA	GTTCCCTCTAC	CGTCAGAACG	ACGCAGATTT	TCAATATTGG	660
GAATATCTCG	GGCAATGGTG	GAAGGAGCCC	CTTAATACCA	CTTGGGGAAA	GGGTGACTGG	720
GCCGGGGGTT	GGGGCTTCAA	CTTGAGGTT	GGCAACGTCT	TTAGTCTGAA	TGCAGAGGGG	780
TATAGTGAAG	ACGGCGAGAT	ATTCTATAACC	CTCGGTGCTG	AGGGTTCGGG	ACTTCCCATC	840
GTTCCCTCAAG	TCTCCTCTAT	TCGCGATATG	CTGTGGGTGA	CCGGCAATGT	CACAAATGAC	900
GGCTCTGTCA	CTTTCAAGCC	AACCATGGCG	GGTGTGCTTG	ACTGGGGCGT	GTCGGCATAT	960
GCTGCTGCAG	GCAAGATCTT	GCCGGCCAGC	TCTCAGGCAT	CCACAAAGAG	CGGTGCCCGCC	1020

GATCGGGTCA	TTTCCTATGT	CTGGCTCACT	GGAGATCTAT	TCGAGCAAGT	GAAAGGATT	1080
CCTACCGCTC	AACAAAAC	TG GACCCGGGCC	CTCTTACTGC	CGCGAGAGCT	GAATGTCCGC	1140
ACTATCTCTA	ACGTGGTGGA	TAACGAAC	TT TCGCGTGAGT	CCTTGACATC	GTGGCGCGTG	1200
GCCCCGCGAAG	ACTCTGGTCA	GATCGAC	TTT GAAACAATGG	GAATCTCAAT	TTCCAGGGAG	1260
ACTTACAGCG	CTCTCACATC	CGGCTCATCT	TTTGTGAGT	CTGGTAAAAC	GTTGTCGAAT	1320
GCTGGAGCAG	TGCCCTCAA	TACCTCACCC	TCAAGCAAGT	TCTTCGTGCT	GACAGCAAAT	1380
ATATCTTCC	CGACCTCTGC	CCGTGACTCT	GGCATCCAGG	CTGGTTTCCA	GGTTTTATCC	1440
TCTAGTCTTG	AGTCTACAAAC	TATCTACTAC	CAATTCTCCA	ACGAGTCCAT	CATCGTCGAC	1500
CGCAGCAACA	CGAGTGCTGC	GGCGAGAAC	ACTGCTGGGA	TCCTCAGTGA	TAACGAGGCG	1560
GGACGTCTGC	GCCTCTCGA	CGTGTGCGA	AATGGAAAAG	AACAGGTTGA	AACTTTGGAG	1620
CTCACTATCG	TGGTGGATAA	TAGTGTACTG	GAAGTATATG	CCAATGGACG	CTTGCTCTA	1680
GGCACTTGGG	CTCGG					1695

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Microorganism: *Scopulariopsis brevicaulis* IF04843

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1 .. 574

(C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gln Pro Thr Ser Leu Ser Ile Asp Asn Ser Thr Tyr Pro Ser Ile Asp
1 5 10 15
Tyr Asn Ser Ala Pro Pro Asn Leu Ser Thr Leu Ala Asn Asn Ser Leu
20 25 30
Phe Glu Thr Trp Arg Pro Arg Ala His Val Leu Pro Pro Gln Asn Gln
35 40 45
Ile Gly Asp Pro Cys Met His Tyr Thr Asp Pro Glu Thr Gly Ile Phe
50 55 60
His Val Gly Trp Leu Tyr Asn Gly Asn Gly Ala Ser Gly Ala Thr Thr
65 70 75 80
Glu Asp Leu Val Thr Tyr Gln Asp Leu Asn Pro Asp Gly Ala Gln Met
85 90 95
Ile Leu Pro Gly Gly Val Asn Asp Pro Ile Ala Val Phe Asp Gly Ala
100 105 110
Val Ile Pro Ser Gly Ile Asp Gly Lys Pro Thr Met Met Tyr Thr Ser
115 120 125
Val Ser Tyr Met Pro Ile Ser Trp Ser Ile Ala Tyr Thr Arg Gly Ser
130 135 140
Glu Thr His Ser Leu Ala Val Ser Ser Asp Gly Gly Lys Asn Phe Thr
145 150 155 160
Lys Leu Val Gln Gly Pro Val Ile Pro Ser Pro Pro Phe Gly Ala Asn
165 170 175

Val Thr Ser Trp Arg Asp Pro Phe Leu Phe Gln Asn Pro Gln Phe Asp
180 185 190
Ser Leu Leu Glu Ser Glu Asn Gly Thr Trp Tyr Thr Val Ile Ser Gly
195 200 205
Gly Ile His Gly Asp Gly Pro Ser Ala Phe Leu Tyr Arg Gln His Asp
210 215 220
Pro Asp Phe Gln Tyr Trp Glu Tyr Leu Gly Pro Trp Trp Asn Glu Glu
225 230 235 240
Gly Asn Ser Thr Trp Gly Ser Gly Asp Trp Ala Gly Arg Trp Gly Tyr
245 250 255
Asn Phe Glu Val Ile Asn Ile Val Gly Leu Asp Asp Asp Gly Tyr Asn
260 265 270
Pro Asp Gly Glu Ile Phe Ala Thr Val Gly Thr Glu Trp Ser Phe Asp
275 280 285
Pro Ile Lys Pro Gln Ala Ser Asp Asn Arg Glu Met Leu Trp Ala Ala
290 295 300
Gly Asn Met Thr Leu Glu Asp Gly Asp Ile Lys Phe Thr Pro Ser Met
305 310 315 320
Ala Gly Tyr Leu Asp Trp Gly Leu Ser Ala Tyr Ala Ala Ala Gly Lys
325 330 335
Glu Leu Pro Ala Ser Ser Lys Pro Ser Gln Lys Ser Gly Ala Pro Asp
340 345 350
Arg Phe Val Ser Tyr Leu Trp Leu Thr Gly Asp Tyr Phe Glu Gly His
355 360 365

Asp Phe Pro Thr Pro Gln Gln Asn Trp Thr Gly Ser Leu Leu Leu Pro
370 375 380

Arg Glu Leu Ser Val Gly Thr Ile Pro Asn Val Val Asp Asn Glu Leu
385 390 395 400

Ala Arg Glu Thr Gly Ser Trp Arg Val Gly Thr Asn Asp Thr Gly Val
405 410 415

Leu Glu Leu Val Thr Leu Lys Gln Glu Ile Ala Arg Glu Thr Leu Ala
420 425 430

Glu Met Thr Ser Gly Asn Ser Phe Thr Glu Ala Ser Arg Asn Val Ser
435 440 445

Ser Pro Gly Ser Thr Ala Phe Gln Gln Ser Leu Asp Ser Lys Phe Phe
450 455 460

Val Leu Thr Ala Ser Leu Ser Phe Pro Ser Ser Ala Arg Asp Ser Asp
465 470 475 480

Leu Lys Ala Gly Phe Glu Ile Leu Ser Ser Glu Phe Glu Ser Thr Thr
485 490 495

Val Tyr Tyr Gln Phe Ser Asn Glu Ser Ile Ile Ile Asp Arg Ser Asn
500 505 510

Ser Ser Ala Ala Ala Leu Thr Thr Asp Gly Ile Asp Thr Arg Asn Glu
515 520 525

Phe Gly Lys Met Arg Leu Phe Asp Val Val Glu Gly Asp Gln Glu Arg
530 535 540

Ile Glu Thr Leu Asp Leu Thr Ile Val Val Asp Asn Ser Ile Val Glu
545 550 555 560

Val His Ala Asn Gly Arg Phe Ala Leu Ser Thr Trp Val Arg

565

570

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1722 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double stranded
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Microorganism: Scopulariopsis brevicaulis IFO4843

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1 .. 1722
- (C) IDENTIFICATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAACCTACGT CTCTGTCAAT CGACAATTCC ACGTATCCTT CTATCGACTA CAACTCCGCC	60
CCTCCAAACC TCTCGACTCT TGCCAACAAC AGCCTCTTCG AGACATGGAG GCCGAGGGCA	120
CACGTCCCTC CGCCCCAGAA CCAGATCGGC GATCCGTGTA TGCAC TACAC CGACCCCGAG	180
ACAGGAATCT TCCACGTCGG CTGGCTGTAC AACGGCAATG GCGCTTCCGG CGCCACGACC	240
GAGGATCTCG TCACCTATCA GGATCTCAAC CCCGACGGAG CGCAGATGAT CCTTCCGGGT	300
GGTGTGAATG ACCCCATTGC TGTCTTGAC GGCGCGGTTA TTCCCAGTGG CATTGATGGG	360
AAACCCACCA TGATGTATACTCGGTGTCA TACATGCCA TCTCCTGGAG CATCGCTTAC	420
ACCAGGGGAA GCGAGACCCA CTCTCTCGCA GTGTCGTCCG ACGGCGGTAA GAACTTCACC	480

AAGCTGGTGC	AGGGCCCCGT	CATTCCCTCG	CCTCCCTTCG	GCGCCAACGT	GACCAGCTGG	540
CGTGACCCCT	TCCTGTTCCA	AAACCCCCAG	TTCGACTCTC	TCCTCGAAAG	CGAGAACGGC	600
ACGTGGTACA	CCGTTATCTC	TGGTGGCATC	CACGGTGACG	GCCCCTCCGC	GTTCCCTCTAC	660
CGTCAGCACG	ACCCCGACTT	CCAGTACTGG	GAGTACCTTG	GACCGTGGTG	GAACGAGGAA	720
GGGAACTCGA	CCTGGGGCAG	CGGTGACTGG	GCTGGCCGGT	GGGGCTACAA	CTTCGAGGTC	780
ATCAACATTG	TCGGTCTTGA	CGATGATGGC	TACAACCCCCG	ACGGTCAAAT	CTTGCCACG	840
GTAGGTACCG	AATGGTCGTT	TGACCCCATC	AAACCGCAGG	CCTCGGACAA	CAGGGAGATG	900
CTCTGGGCCG	CGGGCAACAT	GAECTCTCGAG	GACGGCGATA	TCAAGTTCAC	GCCAAGCATG	960
GCAGGGCTACC	TCGACTGGGG	TCTATCGGCG	TATGCCGCCG	CTGGCAAGGA	GCTGCCCGCT	1020
TCTTCAAAGC	CTTCGCAGAA	GAGCGGTGCG	CCGGACCGGT	TCGTGTCGTA	CCTGTGGCTC	1080
ACCGGTGACT	ACTTCGAGGG	CCACGACTTC	CCCACCCCGC	AGCAGAATTG	GACCGGCTCG	1140
CTTTGCTTC	CGCGTGAGCT	GAGCGTGGG	ACGATTCCA	ACGTTGTCGA	CAACGAGCTT	1200
GCTCGCGAGA	CGGGCTCTTG	GAGGGTTGGC	ACCAACGACA	CTGGCGTGCT	TGAGCTGGTC	1260
ACTCTGAAGC	AGGAGATTGC	TCGCGAGACG	CTGGCTGAAA	TGACCAGCGG	CAAECTCCTTC	1320
ACCGAGGCGA	GCAGGAATGT	CAGCTGCC	GGATCTACCG	CCTTCCAGCA	GTCCCTGGAT	1380
TCCAAGTTCT	TCGTCCTGAC	CGCCTCGCTC	TCCTTCCCTT	CGTCGGCTCG	CGACTCCGAC	1440
CTCAAGGCTG	GTTCGAGAT	CCTGTCGTCC	GAGTTGAGT	CGACCACGGT	CTACTACCAG	1500
TTTTCCAACG	AGTCCATCAT	CATTGACCGG	AGCAACTCGA	GTGCTGCCGC	CTTGACTACC	1560
GATGGAATCG	ACACCCGCAA	CGAGTTGGC	AAGATGCGCC	TGTTGATGT	TGTCGAGGGT	1620
GACCAGGAGC	GTATCGAGAC	GCTCGATCTC	ACTATTGTGG	TTGATAACTC	GATCGTTGAG	1680
GTTCATGCCA	ACGGGCGATT	CGCTCTGAGC	ACTTGGGTTTC	GG		1722

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

- (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GC₂GAATTCCA ATGAAGCTCA CCACTACC

28

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGGATCCCC GTCAATTCT CTCC

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTGACCGG TGTTCATCC

19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCGGGTTGTC ATAGATGTGG

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAATCCAGGA GGATCCCAAT GAAG

24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGACCGGGAT CCGGGCATGC AG

22

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGCGTCGTCT AGAGGTTGTC ACTT

24

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCTATTGGG GTCCATGGCC C

21

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAACTGCTGG CATCCTCAGT GA

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGGATCCAT GAAGCTATCA AATGCAATCA

30

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GC GGATCCTT ACCGAGCCCCA AGTGCC

26

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GC GGATCCAA TGAAGCTCAC CACTACC

27

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCGGATCCCC GTCAATTCT CTCC

24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCACCGCCT GGCGCGATCC G

21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCACGGAGT GGTCTGGCC

19

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTCCAGTATC AAGGATATGC TGTG

24

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGACCAGTAC AAGCAGGCCGG

20

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Not relevant
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCCAGTATCC GCGATATGCT G

21

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGCACGGAG GTTTCTGGCC TGC

23

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGGCACGGAG GAGTCTGGCC TGC

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Not relevant
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGGCACGGAG GATTCTGGCC TGC

23